



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/675,072
Source: ORF
Date Processed by STIC: 10-10-03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003



IFWO

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/675,072

DATE: 10/10/2003
 TIME: 14:43:39

Input Set : A:\1288R SEQLIST.TXT
 Output Set: N:\CRF4\10102003\J675072.raw

**Does Not Comply
 Corrected Diskette Needed**

4 <110> APPLICANT: Yumin, Tao
 5 Gordon-Kamm, William
 6 Shen, Bo
 7 Lowe, Keith
 8 Danilevskaya, Olga
 9 Mahajan, Pramod
 10 Rafalski, Jan Antoni
 11 Sakai, Hajime
 12 Klein, Theodore
 15 <120> TITLE OF INVENTION: Transcriptional Regulatory Nucleic
 16 Acids, Polypeptides, and Methods of Use Thereof
 19 <130> FILE REFERENCE: 1288R
 C--> 21 <140> CURRENT APPLICATION NUMBER: US/10/675,072
 C--> 21 <141> CURRENT FILING DATE: 2003-09-30
 21 <150> PRIOR APPLICATION NUMBER: 10/005,057
 22 <151> PRIOR FILING DATE: 2001-12-04
 24 <150> PRIOR APPLICATION NUMBER: 60/251,555
 25 <151> PRIOR FILING DATE: 2000-12-06
 27 <160> NUMBER OF SEQ ID NOS: 43
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1874
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Zea mays
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (3)...(1655)
 40 <400> SEQUENCE: 1
 41 ac gag aat gat gaa tct cgc caa att cat tat gac gaa gct gca att 47
 42 Glu Asn Asp Glu Ser Arg Gln Ile His Tyr Asp Glu Ala Ala Ile
 43 1 5 10 15
 45 gag agg ttg tta gac cgt gat caa gtt gac ggt gat gaa tct gtg gaa 95
 46 Glu Arg Leu Leu Asp Arg Asp Gln Val Asp Gly Asp Glu Ser Val Glu
 47 20 25 30
 49 gat gaa gaa gaa gat gga ttc tta aaa gga ttc aag gtt gca aac ttt 143
 50 Asp Glu Glu Glu Asp Gly Phe Leu Lys Gly Phe Lys Val Ala Asn Phe
 51 35 40 45
 53 gaa tat atc gat gag gca aag gct cag gca gaa aaa gag gag gca cgg 191
 54 Glu Tyr Ile Asp Glu Ala Lys Ala Gln Ala Glu Lys Glu Glu Ala Arg
 55 50 55 60
 57 aga aag gct gca gct gag gct gaa aat tct gaa aga aac tac tgg gat 239
 58 Arg Lys Ala Ala Ala Glu Ala Glu Asn Ser Glu Arg Asn Tyr Trp Asp
 59 65 70 75

P. 5-6

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61	gaa	cta	ttg	aag	gat	aga	tat	gat	gta	cag	aaa	gtt	gaa	gaa	cat	act	287
62	Glu	Leu	Leu	Lys	Asp	Arg	Tyr	Asp	Val	Gln	Lys	Val	Glu	Glu	His	Thr	
63	80					85					90					95	
65	gct	atg	gga	aaa	ggg	aaa	aga	agc	cgc	aaa	cag	atg	gct	gcc	gct	gat	335
66	Ala	Met	Gly	Lys	Gly	Lys	Arg	Ser	Arg	Lys	Gln	Met	Ala	Ala	Ala	Asp	
67					100					105					110		
69	gaa	gat	gac	att	cat	gat	tta	agt	tcc	gaa	gat	gag	gat	tac	tca	ttg	383
70	Glu	Asp	Asp	Ile	His	Asp	Leu	Ser	Ser	Glu	Asp	Glu	Asp	Tyr	Ser	Leu	
71				115					120					125			
73	gag	gat	gac	att	tca	gat	aat	gac	aca	agt	ttg	caa	gga	aat	att	tct	431
74	Glu	Asp	Asp	Ile	Ser	Asp	Asn	Asp	Thr	Ser	Leu	Gln	Gly	Asn	Ile	Ser	
75				130				135					140				
77	ggg	aag	agg	gga	caa	tat	tct	aag	aga	aaa	tca	cgt	aat	gtt	gat	tct	479
78	Gly	Lys	Arg	Gly	Gln	Tyr	Ser	Lys	Arg	Lys	Ser	Arg	Asn	Val	Asp	Ser	
79				145			150				155						
81	att	cca	ttg	atg	gag	ggc	gaa	gga	cgt	acc	ttg	aga	gtt	ctt	gga	ttc	527
82	Ile	Pro	Leu	Met	Glu	Gly	Glu	Gly	Arg	Thr	Leu	Arg	Val	Leu	Gly	Phe	
83	160					165					170					175	
85	aac	cat	gct	caa	cga	gca	atg	ttc	cta	cag	aca	ctc	aat	aga	ttc	ggt	575
86	Asn	His	Ala	Gln	Arg	Ala	Met	Phe	Leu	Gln	Thr	Leu	Asn	Arg	Phe	Gly	
87					180				185					190			
89	ttt	cag	aat	tat	gac	tg	aaa	gag	tat	ctt	cct	cgt	ctt	aaa	gga	aaa	623
90	Phe	Gln	Asn	Tyr	Asp	Trp	Lys	Glu	Tyr	Leu	Pro	Arg	Leu	Lys	Gly	Lys	
91				195					200					205			
93	agt	gtc	gag	gaa	atc	cag	aga	tat	gct	gaa	ctt	gtc	atg	gca	cat	ctt	671
94	Ser	Val	Glu	Glu	Ile	Gln	Arg	Tyr	Ala	Glu	Leu	Val	Met	Ala	His	Leu	
95				210			215				220						
97	gtt	gaa	gaa	att	aat	gat	tct	gac	tat	ttt	tca	gat	ggc	gtt	cca	aag	719
98	Val	Glu	Glu	Ile	Asn	Asp	Ser	Asp	Tyr	Phe	Ser	Asp	Gly	Val	Pro	Lys	
99				225			230				235						
101	gaa	atg	atg	cgt	gtt	gat	gat	gta	cta	gtc	agg	ata	gca	aac	ata	tcc	767
102	Glu	Met	Met	Arg	Val	Asp	Asp	Val	Leu	Val	Arg	Ile	Ala	Asn	Ile	Ser	
103	240					245					250				255		
105	ctt	atc	gag	gag	aag	atg	gct	gcc	aca	gga	cca	gga	aaa	att	aca	aac	815
106	Leu	Ile	Glu	Glu	Lys	Met	Ala	Ala	Thr	Gly	Pro	Gly	Lys	ile	Thr	Asn	
107					260				265					270			
109	att	ttt	cct	aat	tac	ttg	ctc	tat	gag	ttc	caa	ggc	tta	tct	ggt	gga	863
110	Ile	Phe	Pro	Asn	Tyr	Leu	Leu	Tyr	Glu	Phe	Gln	Gly	Leu	Ser	Gly	Gly	
111				275				280					285				
113	aga	ata	tg	aaa	gcg	gag	cat	gat	cta	ctg	tta	ctg	aga	ggc	ata	ctg	911
114	Arg	Ile	Trp	Lys	Ala	Glu	His	Asp	Leu	Leu	Leu	Leu	Arg	Gly	Ile	Leu	
115				290				295					300				
117	aag	cat	gga	tat	gca	agg	tg	cag	tat	ata	tca	gat	gac	aga	gag	aat	959
118	Lys	His	Gly	Tyr	Ala	Arg	Trp	Gln	Tyr	Ile	Ser	Asp	Arg	Gly	Glu	Asn	
119				305			310					315					
121	ggg	ctt	ttt	gag	gct	gca	cga	cga	gag	ctg	cat	ctc	cct	tcg	gtt	aat	1007
122	Gly	Leu	Phe	Glu	Ala	Ala	Arg	Arg	Glu	Leu	His	Leu	Pro	Ser	Val	Asn	
123	320					325					330					335	
125	gaa	ata	att	ggt	gct	cag	ttg	aac	gag	gca	aat	ggg	aat	ttg	gaa	ggt	1055

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Input Set : A:\1288R SEQLIST.TXT

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126 Glu Ile Ile Gly Ala Gln Leu Asn Glu Ala Asn Gly Asn Leu Glu Gly
127                               340           345           350
129 gca cag gaa ggc caa gcg aac aca aca agc atg tcg cat tac aag gag      1103
130 Ala Gln Glu Gly Gln Ala Asn Thr Thr Ser Met Ser His Tyr Lys Glu
131                               355           360           365
133 atc cag aga aag ata gtt gag ttc ttg aga aag aga tat cat ctt atg      1151
134 Ile Gln Arg Lys Ile Val Glu Phe Leu Arg Lys Arg Tyr His Leu Met
135                               370           375           380
137 gag aga gcc ttg aat ctg gaa tat gct gtg ata aag aaa aaa att cct      1199
138 Glu Arg Ala Leu Asn Leu Glu Tyr Ala Val Ile Lys Lys Lys Ile Pro
139                               385           390           395
141 gtt cct gat gat att act gaa caa ggt gtt cca gca gga cat gct ccg      1247
142 Val Pro Asp Asp Ile Thr Glu Gln Gly Val Pro Ala Gly His Ala Pro
143 400                               405           410           415
145 ctt att cca gat atc agt gaa ctg ttg cgg gaa ttg ccc aat ctt gag      1295
146 Leu Ile Pro Asp Ile Ser Glu Leu Leu Arg Glu Leu Pro Asn Leu Glu
147                               420           425           430
149 cca att tct acc aat gaa ttg att tct gag ggc aca gct ggt cag tta      1343
150 Pro Ile Ser Thr Asn Glu Leu Ile Ser Glu Gly Thr Ala Gly Gln Leu
151                               435           440           445
153 caa gtt ccc cat ctc tac aat aag atg tgt gga gtg ctt gaa gag agt      1391
154 Gln Val Pro His Leu Tyr Asn Lys Met Cys Gly Val Leu Glu Glu Ser
155                               450           455           460
157 ggt gct tat gcg ctc agt tcc ttc ttt gga gac aag tcc gca tct tct      1439
158 Gly Ala Tyr Ala Leu Ser Ser Phe Phe Gly Asp Lys Ser Ala Ser Ser
159                               465           470           475
161 act ttg gcc aat agc ctt cga cag ttt gaa act gtg tgt gag aat gtc      1487
162 Thr Leu Ala Asn Ser Leu Arg Gln Phe Glu Thr Val Cys Glu Asn Val
163 480                               485           490           495
165 gtc gag gcc tta cga cca cac caa aat ggt act gcc agt gcc atc aaa      1535
166 Val Glu Ala Leu Arg Pro His Gln Asn Gly Thr Ala Ser Ala Ile Lys
167                               500           505           510
169 gag gaa ttg gta gat gca gcc acc aaa gca gca gca gca gct cct      1583
170 Glu Glu Leu Val Asp Ala Ala Thr Lys Ala Ala Ala Ala Ala Pro
171                               515           520           525
173 caa caa gat tca ggc cat gat gca ccg cat ggg cag tct tcg aca gcc      1631
174 Gln Gln Asp Ser Gly His Asp Ala Pro His Gly Gln Ser Ser Thr Ala
175                               530           535           540
177 aag gcg gac atg gaa atc gat ggt tgattttgat gttccagagt ggcaagaaa      1685
178 Lys Ala Asp Met Glu Ile Asp Gly
179                               545           550
181 ggaatccctt ctaatcatta tgtatactgt ggtcagaatg tccgctatat attgtaacat      1745
182 caaagaaaag acctccaggc ctgaggggtgt tactgtctaata gcgtttggtt tacttgtcct      1805
183 tgtaatatgc atacacattt agaactcatg cagccattgt gtgaaaaaaa aaaaaaaaaa      1865
184 aaaaaaaaaa
186 <210> SEQ ID NO: 2
187 <211> LENGTH: 551
188 <212> TYPE: PRT
189 <213> ORGANISM: Zea mays

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191 <400> SEQUENCE: 2
192 Glu Asn Asp Glu Ser Arg Gln Ile His Tyr Asp Glu Ala Ala Ile Glu
193 1 5 10 15
194 Arg Leu Leu Asp Arg Asp Gln Val Asp Gly Asp Glu Ser Val Glu Asp
195 20 25 30
196 Glu Glu Glu Asp Gly Phe Leu Lys Gly Phe Lys Val Ala Asn Phe Glu
197 35 40 45
198 Tyr Ile Asp Glu Ala Lys Ala Gln Ala Glu Lys Glu Glu Ala Arg Arg
199 50 55 60
200 Lys Ala Ala Ala Glu Ala Glu Asn Ser Glu Arg Asn Tyr Trp Asp Glu
201 65 70 75 80
202 Leu Leu Lys Asp Arg Tyr Asp Val Gln Lys Val Glu Glu His Thr Ala
203 85 90 95
204 Met Gly Lys Gly Lys Arg Ser Arg Lys Gln Met Ala Ala Asp Glu
205 100 105 110
206 Asp Asp Ile His Asp Leu Ser Ser Glu Asp Glu Asp Tyr Ser Leu Glu
207 115 120 125
208 Asp Asp Ile Ser Asp Asn Asp Thr Ser Leu Gln Gly Asn Ile Ser Gly
209 130 135 140
210 Lys Arg Gly Gln Tyr Ser Lys Arg Lys Ser Arg Asn Val Asp Ser Ile
211 145 150 155 160
212 Pro Leu Met Glu Gly Glu Gly Arg Thr Leu Arg Val Leu Gly Phe Asn
213 165 170 175
214 His Ala Gln Arg Ala Met Phe Leu Gln Thr Leu Asn Arg Phe Gly Phe
215 180 185 190
216 Gln Asn Tyr Asp Trp Lys Glu Tyr Leu Pro Arg Leu Lys Gly Lys Ser
217 195 200 205
218 Val Glu Glu Ile Gln Arg Tyr Ala Glu Leu Val Met Ala His Leu Val
219 210 215 220
220 Glu Glu Ile Asn Asp Ser Asp Tyr Phe Ser Asp Gly Val Pro Lys Glu
221 225 230 235 240
222 Met Met Arg Val Asp Asp Val Leu Val Arg Ile Ala Asn Ile Ser Leu
223 245 250 255
224 Ile Glu Glu Lys Met Ala Ala Thr Gly Pro Gly Lys Ile Thr Asn Ile
225 260 265 270
226 Phe Pro Asn Tyr Leu Leu Tyr Glu Phe Gln Gly Leu Ser Gly Gly Arg
227 275 280 285
228 Ile Trp Lys Ala Glu His Asp Leu Leu Leu Arg Gly Ile Leu Lys
229 290 295 300
230 His Gly Tyr Ala Arg Trp Gln Tyr Ile Ser Asp Asp Arg Glu Asn Gly
231 305 310 315 320
232 Leu Phe Glu Ala Ala Arg Arg Glu Leu His Leu Pro Ser Val Asn Glu
233 325 330 335
234 Ile Ile Gly Ala Gln Leu Asn Glu Ala Asn Gly Asn Leu Glu Gly Ala
235 340 345 350
236 Gln Glu Gly Gln Ala Asn Thr Thr Ser Met Ser His Tyr Lys Glu Ile
237 355 360 365
238 Gln Arg Lys Ile Val Glu Phe Leu Arg Lys Arg Tyr His Leu Met Glu
239 370 375 380

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Output Set: N:\CRF4\10102003\J675072.raw

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240 Arg Ala Leu Asn Leu Glu Tyr Ala Val Ile Lys Lys Lys Ile Pro Val
241 385 390 395 400
242 Pro Asp Asp Ile Thr Glu Gln Gly Val Pro Ala Gly His Ala Pro Leu
243 405 410 415
244 Ile Pro Asp Ile Ser Glu Leu Leu Arg Glu Leu Pro Asn Leu Glu Pro
245 420 425 430
246 Ile Ser Thr Asn Glu Leu Ile Ser Glu Gly Thr Ala Gly Gln Leu Gln
247 435 440 445
248 Val Pro His Leu Tyr Asn Lys Met Cys Gly Val Leu Glu Glu Ser Gly
249 450 455 460
250 Ala Tyr Ala Leu Ser Ser Phe Phe Gly Asp Lys Ser Ala Ser Ser Thr
251 465 470 475 480
252 Leu Ala Asn Ser Leu Arg Gln Phe Glu Thr Val Cys Glu Asn Val Val
253 485 490 495
254 Glu Ala Leu Arg Pro His Gln Asn Gly Thr Ala Ser Ala Ile Lys Glu
255 500 505 510
256 Glu Leu Val Asp Ala Ala Thr Lys Ala Ala Ala Ala Pro Gln
257 515 520 525
258 Gln Asp Ser Gly His Asp Ala Pro His Gly Gln Ser Ser Thr Ala Lys
259 530 535 540
260 Ala Asp Met Glu Ile Asp Gly
261 545 550

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263 <210> SEQ ID NO: 3

264 <211> LENGTH: 21

265 <212> TYPE: DNA

266 <213> ORGANISM: Artificial Sequence

268 <220> FEATURE:

269 <221> NAME/KEY: primer_bind

270 <222> LOCATION: (1)...(21)

W--> 272 <223> OTHER INFORMATION:

W--> 272 <400> 3

273 acgagaatga tgaatctgc c

275 <210> SEQ ID NO: 4

276 <211> LENGTH: 23

277 <212> TYPE: DNA

278 <213> ORGANISM: Artificial Sequence

280 <220> FEATURE:

281 <221> NAME/KEY: primer_bind

282 <222> LOCATION: (1)...(23)

W--> 284 <223> OTHER INFORMATION:

W--> 284 <400> 4

285 tcaaccatcg atttccatgt ccg

287 <210> SEQ ID NO: 5

288 <211> LENGTH: 941

289 <212> TYPE: DNA

290 <213> ORGANISM: Zea mays

292 <220> FEATURE:

293 <221> NAME/KEY: CDS

294 <222> LOCATION: (48)...(938)

21

23

See page 6 on error
summary report.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 429,1443
Seq#:13; Xaa Pos. 143,481
Seq#:14; Xaa Pos. 143,481
Seq#:17; N Pos. 260
Seq#:17; Xaa Pos. 87
Seq#:18; Xaa Pos. 87
Seq#:21; N Pos. 3,25,27,114
Seq#:21; Xaa Pos. 7,8,37
Seq#:22; Xaa Pos. 7,8,37
Seq#:25; N Pos. 8,10,15,31,48,62,79,181,194
Seq#:29; N Pos. 463,510
Seq#:29; Xaa Pos. 155,170
Seq#:30; Xaa Pos. 153,167
Seq#:37; N Pos. 543,566,568,575,597,608,621,647,657,659,667
Seq#:37; Xaa Pos. 181,189,192,199,203,207,216,219,220,222
Seq#:38; Xaa Pos. 176,183,186,192,196,200,209,211,212,214
Seq#:41; N Pos. 11757,11808,11859

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:3,4,7,8,11,12,15,16,19,20,23,24,27,28,31,32,35,36,39,40

VERIFICATION SUMMARY
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L:21 M:270 C: Current Application Number differs, Replaced Current Application No
 L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:272 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
 ORGANISM:Artificial Sequence
 L:272 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:272
 L:284 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
 ORGANISM:Artificial Sequence
 L:284 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:284
 L:437 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
 ORGANISM:Artificial Sequence
 L:437 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:437
 L:449 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
 ORGANISM:Artificial Sequence
 L:449 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:449
 L:719 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
 ORGANISM:Artificial Sequence
 L:719 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:719
 L:731 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
 ORGANISM:Artificial Sequence
 L:731 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:731
 L:747 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13
 L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:383
 M:341 Repeated in SeqNo=13
 L:900 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:128
 M:341 Repeated in SeqNo=14
 L:956 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
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 L:956 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:956
 L:968 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
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 L:968 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:968
 L:984 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17
 L:1005 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:241
 M:341 Repeated in SeqNo=17
 L:1147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:80
 L:1217 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
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 L:1217 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:1217
 L:1229 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
 ORGANISM:Artificial Sequence
 L:1229 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:1229
 L:1245 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
 L:1246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
 M:341 Repeated in SeqNo=21
 L:1302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
 M:341 Repeated in SeqNo=22
 L:1334 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
 ORGANISM:Artificial Sequence
 L:1334 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1334
 L:1346 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
 ORGANISM:Artificial Sequence
 L:1346 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:1346
 L:1362 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25

L:1363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:1416 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:1416 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:1416
L:1428 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:28, <213>
ORGANISM:Artificial Sequence
L:1428 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:1428
L:1444 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29

VERIFICATION SUMMARY

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Input Set : A:\1288R SEQLIST.TXT

Output Set: N:\CRF4\10102003\J675072.raw

L:1481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:432
 M:341 Repeated in SeqNo=29
 L:1519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:144
 M:341 Repeated in SeqNo=30
 L:1533 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
 ORGANISM:Artificial Sequence
 L:1533 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:1533
 L:1545 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
 ORGANISM:Artificial Sequence
 L:1545 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:1545
 L:1641 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:35, <213>
 ORGANISM:Artificial Sequence
 L:1641 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:1641
 L:1653 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:36, <213>
 ORGANISM:Artificial Sequence
 L:1653 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:36,Line#:1653
 L:1669 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37
 L:1714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:529
 M:341 Repeated in SeqNo=37
 L:1758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:160
 M:341 Repeated in SeqNo=38
 L:1776 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:39, <213>
 ORGANISM:Artificial Sequence
 L:1776 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:39,Line#:1776
 L:1788 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:40, <213>
 ORGANISM:Artificial Sequence
 L:1788 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:40,Line#:1788
 L:1805 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41
 L:2001 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:11700
 M:341 Repeated in SeqNo=41